#### **FULL LENGTH APO-A1 SEQUENCE**

1
MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE

TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE

194
LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHA
267
KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ (SEQ ID NO:2)

sig\_peptide 20..91
mature\_protein 92..820

20 a tgaaagctgc ggtgctgacc ttggccgtgc tcttcctgac

61 ggggagccag geteggeatt tetggeagca agatgaacce ceceagagce cetgggateg
121 agtgaaggac etggecaetg tgtacgtgga tgtgeteaaa gacageggca gagactatgt
181 gteceagttt gaaggeteeg cettgggaaa acagetaaac etaaagetee ttgacaactg
241 ggacagegtg acetecacet teagcaaget gegegaacag eteggeeetg tgaceeagga
301 gttetgggat aacetggaaa aggagacaga gggeetgagg caggagatga geaaggatet
361 ggaggaggtg aaggeeaagg tgeageeeta eetggacgae tteeagaaga agtggeagga
421 ggagatggag etetacegee agaaggtgga geegetgege geagagetee aagagggege
481 gegeeagaag etgcaegage tgeaagaaa getgageeea etgggegagg agatgegea
541 eegeggege geeeatgtgg aegegetgeg eacgeatetg geeeeetaca gegaegget
601 gegeeagege ttggeegge geettgagge teteaaggag aacggegge eeagaetge
661 egagtaceae geeaaggeea eegageatet gageaegete agegagaagg ceaageeege
721 getegaggae eteegeeaag geetgetgee egtgetggag agetteaagg teagetteet
781 gagegetete gaggagtaca etaagaaget caacacecag (SEQ ID NO:1)

# FIG. 1A

#### 18K N-TERMINAL FRAGMENT

25 DEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE 194 LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL (SEQ ID NO:3)

- 92 gatgaaccc ccccagagcc cctgggatcg
- agtgaaggac ctggccactg tgtacgtga tgtgctcaaa gacagcggca gagactatgt gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga 301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga 421 ggagatggag ctctaccgcc agaaggtgga gccgctgcgc gcagagctcc aagagggcgc 481 gcgccagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga 541 ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgact 601 g (SEQ ID NO:4)

# FIG. 1B

#### 13K N-TERMINAL FRAGMENT

25 DEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE 144 TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE (PORTION OF SEQ ID NO:3)

- 92 gatgaaccc ccccagagcc cctgggatcg
- 121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt
- 181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg
- 241 ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga
- 301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct
- 361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga
- 421 ggagatggag ctctaccgcc agaaggtgga g (PORTION OF SEQ ID NO:4)

# FIG. 1C

### 13K C-TERMINAL FRAGMENT

156 QKLHE

LQEKLSPLGEEMRD RARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHA
267
KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ (PORTION OF SEQ ID NO:2)

cagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga
ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgagct
gcgccagcgc ttggccgcgc gccttgaggc tctcaaggag aacggcggcg ccagactggc
cgagtaccac gccaaggcca ccgagcatct gagcacgctc agcgagaagg ccaagcccgc
gctcgaggac ctccgccaag gcctgctgcc cgtgctggag agcttcaagg tcagcttcct
gagcgctctc gaggagtaca ctaagaagct caacacccag (PORTION OF SEQ ID NO:1)